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Use of melon landraces in integrated breeding through the application of traditional and biotechnological methods

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ABSTRACT

Background: In Armenia, melon (*Cucumis melo* L.) is traditionally cultivated, including both modern cultivars and traditional landrace forms. Increasing demand, changing market conditions, and climate change underscore the need to develop new genotypes. Local landraces represent a valuable genetic resource for breeding due to their genetic diversity, superior taste and quality traits, adaptation to local conditions, and resilience to environmental stresses. These characteristics highlight the potential of modern breeding approaches to accelerate the generation of diverse genotypic material and expand breeding programs.

Objective: Development and evaluation of new promising regenerant melon lines with enhanced yield, improved quality traits, and high adaptability to local soil and climatic conditions, using the landrace melon Meghrashaghik as a valuable genetic resource and combining conventional breeding methods with biotechnological approaches.

Methods: The study was conducted at the Laboratory of Plant Biotechnology, Phytopathology, and Biochemistry and at the experimental plots of SCVIC ME of RA during 2023-2025. The landrace melon Meghrashaghik was used as the starting material. To obtain regenerant lines, in vitro tissue culture was performed on Murashige and Skoog (MS) medium

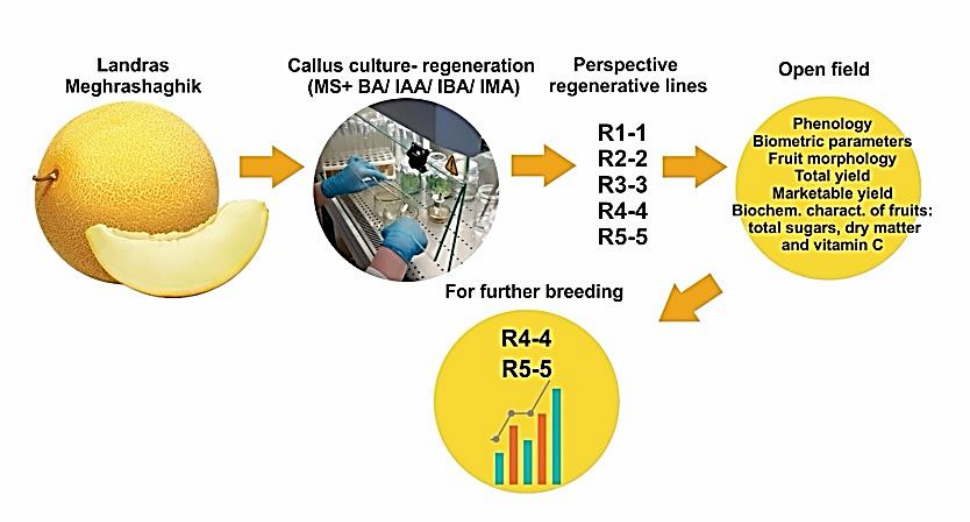
supplemented with phytohormones, depending on the stage of cultivation (callus induction, regeneration, rooting, etc.). Phenological traits and yield were recorded under field conditions throughout the growing season. The biochemical composition of fruits – total sugars and ascorbic acid content – was determined spectrophotometrically, while dry matter content was measured using a refractometer. Statistical analysis was performed using analysis of variance (ANOVA) at $p \leq 0.05$, and mean comparisons were conducted using the least significant difference (LSD) test.

Results: In vitro cultivation produced proliferating and regenerating callus, with a regeneration frequency of 60.1% and rooting of 88.1% in regenerant plants. Somaclonal variation was observed in shoot morphology, growth rate, and leaf coloration, indicating induced genetic variability. Field evaluation of 26 regenerant lines identified five promising lines, with R4-4 and R5-5 showing the strongest overall performance. These lines flowered earlier than the control, showed superior biometric traits, and achieved the highest yields, reaching 287.2–287.3 cwt·ha^{-1}, or 9.3–9.4% above the control. Several regenerants also showed increased sugar and vitamin C content, with the highest values recorded in R4-4. Based on agronomic and biochemical traits, lines R4-4 and R5-5 were selected as the most promising for further breeding.

Novelty of the study: This study is the first to apply an integrated biotechnological approach based on in vitro tissue culture to obtain regenerant lines of the landrace melon Meghrashaghik, followed by field selection of promising genotypes. The use of callus culture and induced morphogenesis enabled the observation of somaclonal variation as a source of genetic diversity, accelerating the generation of new variants with improved biometric traits, higher yield, and enhanced fruit quality. The promising lines R4-4 and R5-5 represent a valuable genetic resource and can serve as starting material for the rapid breeding of high-yielding melon cultivars and hybrids.

Conclusion: The results demonstrate the potential of combining biotechnological and conventional breeding methods in melon selection to accelerate the generation of genetically diverse material and to expand breeding programs.

Keywords: melon, landrace lines, somaclonal variation, regenerant lines, biotechnology, yield, fruit quality, breeding



Graphical Abstract: Use of melon landraces in integrated breeding through the application of traditional and biotechnological methods.

INTRODUCTION

Functional foods are currently a key focus in scientific research and agricultural technologies, as products enriched with bioactive compounds contribute to health promotion and disease prevention [1-3]. Traditional local cultivars represent a valuable source of bioactive compounds and unique quality traits that can be leveraged to enhance the functional value of agricultural products [4-5].

Melon (*Cucumis melo* L.) is one of the most valuable and widely cultivated members of the Cucurbitaceae family in Armenia. Approximately 35-40% of the 4,023 hectares allocated to cucurbit crops in the country is devoted to melon production, highlighting its economic and nutritional significance. Melon is highly appreciated by consumers not only for its distinctive aroma and sweet taste, but also for its considerable nutritional value. Its fruit contains large amounts of water, sugars, proteins, fiber, essential minerals (K, Ca, Mg, Fe, F), and vitamins (C, PP, and B-group), contributing to its beneficial effects on digestion, immunity, and overall health [6-7]. Melon seeds are also valued for their high oil content, which can reach 23–35% and is comparable in quality to olive oil [8]. For centuries, melon has played an important role in both local diets and traditional medicine due to its mild diuretic, anti-inflammatory, antioxidant, and digestive-regulating properties [9].

Armenia has a long history of melon cultivation, dating back to ancient times, particularly in the Ararat Valley. Today, both newly developed varieties and old traditional landraces continue to be grown. Indigenous landraces such as Araratyan, Meghrashaghik, Armaviri, Shiraki, and Yeraskhi remain notable for their high sugar content, strong aroma, drought tolerance, and unique quality characteristics [10]. Despite their value, the diversity of melon varieties officially registered in Armenia remains limited: only six locally bred varieties are included in the State Register of Plant Variety Protection, three of which were developed between 1980 and 1998 [11]. Farmers also cultivate foreign varieties, yet a clear mismatch persists between grower and consumer demands and the characteristics of the available cultivars. Key desirable traits, including sweetness, early ripening, high yield potential, and good transportability, are still insufficiently met. This creates an urgent need for new, locally adapted, and market-preferred varieties.

Old traditional varieties play a crucial role in maintaining agrobiodiversity and ensuring long-term food security [12]. Armenian melon landraces represent an invaluable component of the national genetic heritage due to their broad genetic diversity, local adaptation, high-quality traits, and tolerance to environmental stresses. Their distinctive phenotypes further enhance their attractiveness for both breeders and markets. The targeted study and utilization of these genetic resources are therefore essential for improving breeding programs and strengthening the resilience of local agriculture.

Traditional breeding methods, although fundamental, are often labor-intensive and time-consuming. To increase the efficiency of developing new varieties, modern breeding increasingly relies on an integrated approach that combines conventional methods with in vitro biotechnological techniques. Such integration accelerates breeding, enhances genetic purity, and facilitates the development of stable, high-quality cultivars adapted to local climatic conditions [13]. This approach is particularly relevant for Armenia, where it is critical to preserve the local gene pool while simultaneously meeting rising consumer demand and coping with climate change [14-15].

Considering these factors, the present study aims to investigate and characterize three Armenian melon landraces and evaluate their potential as genetic resources for breeding. Additionally, the study explores the application of in vitro biotechnological methods to enhance breeding efficiency and support the development of high-yielding, high-quality, and

environmentally resilient melon varieties suited to Armenia's agricultural conditions.

MATERIAL AND METHODS

The research was conducted over a three-year period (2023-2025) at the Laboratory of Plant Biotechnology, Phytopathology and Biochemistry, and at the experimental field of SCVIC ME of RA. The Meghrashaghik melon landrace, previously cultivated in the Ararat region, was used as the plant material.

Biotechnological Methods for Obtaining Regenerant Lines. The introduction into in vitro culture and tissue cultivation was carried out following standard protocols [16]. Experiments were established in two replicates. For the biotechnological experiment, the standard Murashige and Skoog (MS) medium was used, supplemented with auxin- and cytokinin-type growth regulators, depending on the cultivation stage. Explants were cultured in darkness at 25-26 °C with 70% relative humidity. The duration of each callus passage was 3-4 weeks, after which the callus was sequentially transferred for further induction of adventitious shoots.

Shoot induction occurred over 2-3 weeks under a 16-hour photoperiod, with illumination of 3000–4000 lux and a temperature of 25-26 °C. Rooted regenerants were acclimatized under greenhouse conditions, after which the plants were transplanted to the field for further investigation of morphophysiological and biochemical traits.

Field Studies. Field experiments were conducted under open-field conditions from 2023 to 2025 at the experimental plots of SCVIC ME of RA, located in the Darakert village, Ararat Region (40.115018° N, 44.417768° E).

During the growing season, the climate was characterized by a gradual increase in temperatures from moderate spring values to peak summer levels, with pronounced diurnal fluctuations, typical of the arid climate of the Ararat Valley. The hot season lasts from June to September, during which the average daily temperature ranges from 27.7 to 36.2 °C during the day and from 16.2 to 23.0 °C at night (Table 1).

Table 1. Average daily and night-time temperatures by month for 2023–2025 in the Ararat Valley [17]

Year	April	May	June	July	August	September
	day/ night temp, °C	day/ night temp, °C	day/ night temp, °C	day/ night temp, °C	day/ night temp, °C	day/ night temp, °C
2023	20.0 / 10.9	24.3 / 13.9	28.9 / 18.3	33.4 / 21.5	35.8 / 23.0	28.1 / 17.0
2024	23.6 / 12.0	21.9 / 13.1	31.5 / 19.1	32.7 / 21.4	35.3 / 22.3	29.0 / 17.8
2025	19.7 / 10.5	25.0 / 14.5	30.3 / 17.6	34.9 / 21.8	36.2 / 22.9	27.7 / 16.2

Precipitation during the growing season is irregular and generally insufficient; therefore, irrigation was carried out with soil moisture monitoring. The highest number of rainy days in the Ararat Valley occurs in May, with an average precipitation of 23 mm [18].

During 2023-2025, the average daily incoming shortwave solar energy in the Ararat Valley exhibited pronounced seasonal fluctuations. The period of maximum insolation occurred from May 20 to August 26, with average daily energy exceeding 7.0 kWh·m², reaching a peak in July (approximately 8.0 kWh·m²). Concurrently, a high number of sunny days was recorded (Fig. 1), creating favorable conditions for photosynthesis, active biomass accumulation, and optimal growth of cucurbit crops.

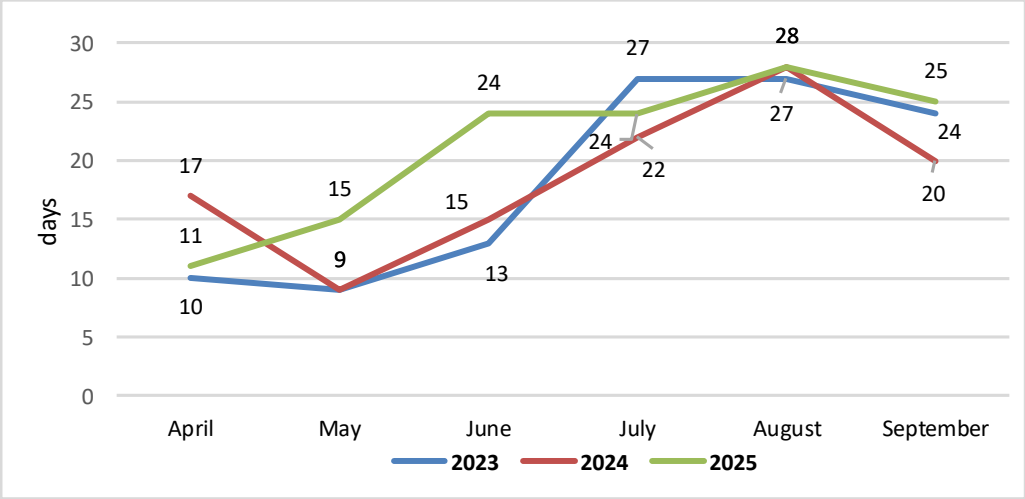


Figure 1. Monthly and annual variation in the number of sunny days in the Ararat Valley [18]

The nutrient content in the root-inhabited soil layer was as follows: total nitrogen (N) - 8.5-12.5mg, available phosphorus (P_2O_5) - 5.0-8.5mg, and potassium (K_2O) - 20.5-30.0mg per 100g of soil. Electrical conductivity (EC) ranged from 1.0 to 1.8dS·m^{-1}, and pH was 6.5-7.5. The plant nutrition system was managed based on soil agrochemical analysis performed using the colorimetric method with a Gallery Aqua Master Discrete Analyzer (Thermo Fisher Scientific) in accordance with ISO 14001:2015 standards.

Experiments were established in four replicates using a 200+80 /2×80 cm planting scheme, with each experimental plot covering 25 m². The local Meghrashaghik cultivar served as the control.

During the growing season, all necessary agronomic practices were applied, including soil cultivation, irrigation, and control of weeds, diseases, and pests. Phenological observations were carried out throughout the vegetation period, recording the number of days from mass emergence to flowering of male and female flowers, as well as to fruit ripening.

The biochemical composition of the fruits was analyzed following standard procedures: total sugars and ascorbic acid content were determined spectrophotometrically, and dry matter content was measured using a refractometer [19]. Yield was determined by the gravimetric method.

Data Analysis: Statistical analysis of the experimental results was performed using analysis of variance (ANOVA) at a significance level of $p \leq 0.05$. The least significant difference (LSD) test was used to compare mean values. Results are presented as means ± standard deviation (SD).

RESULTS AND DISCUSSION

In Vitro Culture and Somaclonal Variation. To establish an in vitro culture, seeds of the melon Meghrashaghik were sterilized in a 15% hydrogen peroxide solution for 15 minutes and then placed on hormone-free Murashige and Skoog (MS) basal medium for germination. Cotyledons with 2-3 mm hypocotyls from 5-6-day-old in vitro-germinated seedlings were used as explants.

For callus induction and subsequent plant regeneration, explants were transferred to a modified MS medium containing 1.0 mg·L^{-1} 6-benzylaminopurine (BA) and 0.1 mg·L^{-1} α-naphthaleneacetic acid (NAA), providing an optimal cytokinin-to-auxin ratio for callus formation. Callus development was accompanied by active growth and subsequent morphogenesis, leading to the formation of adventitious shoots.

For callus amplification, the same hormone combination was used with periodic subculturing every 3-4 weeks, which helped maintain cellular activity and

preserve morphogenetic potential. On this medium, the average number of explants forming callus was 46.5, those producing shoots was 28.1, and the regeneration frequency reached 60.1%.

After 2-3 weeks, the developed shoots were transferred to MS medium supplemented with 0.5 mg·L^{-1} BA and 0.5 mg·L^{-1} indole-3-acetic acid (IAA) for further growth and development.

Shoot rooting was performed on MS medium containing 2.0 mg·L^{-1} indole-3-butyric acid (IBA), where a fully developed root system was formed. The average rooting percentage reached 88.1%.

Rooted regenerants were transferred to greenhouse conditions for gradual acclimatization at 25-26 °C and 70% relative humidity. After successful adaptation, plants were transplanted to the field for further investigation of morphophysiological and biochemical traits.

During the study, signs of somaclonal variation were observed among the regenerants, manifested as differences in shoot morphology, growth rate, and leaf coloration. This indicates the potential accumulation of genetic and epigenetic changes in callus tissue during prolonged in vitro culture, which can be utilized as an additional source of variability in breeding programs. The obtained results are consistent with reports from international authors, who note that somaclonal variation is an inherent phenomenon during prolonged in vitro tissue culture and plays an important role as a source of genetic diversity [20]. Variations arising during callus formation and organogenesis may be caused by point mutations, changes in chromosome number or structure, as well as epigenetic modifications, including DNA hypo- or hypermethylation [21].

According to several studies, such changes can lead to morphological, physiological, and biochemical differences between regenerants and donor plants [22]. This phenomenon is widely utilized to broaden the genetic base and obtain new forms with improved agronomic traits [13, 23]. Tissue culture is particularly effective for inducing genetic variability in vegetable crops such as tomato (*Solanum lycopersicum*) [24-27], pepper (*Capsicum annuum*) [28-29], cabbage (*Brassica oleracea*) [30], as well as in grapevine (*Vitis vinifera*) [31], various medicinal plants [22, 32], and others.

Thus, the use of somaclonal variation in melon tissue culture offers promising opportunities for the accelerated generation of starting material with novel agronomically valuable traits, which can serve as a basis for future breeding programs.

Field Studies. Out of 26 R_o regenerant lines obtained through biotechnological experiments, five of the most promising lines - R1-1, R2-2, R3-3, R4-4, and R5-5 - were selected for evaluation under open-field conditions. The favorable climate of the Ararat Valley, characterized by warm summers, diurnal temperature fluctuations, and a high number of sunny days, provides optimal conditions for melon development, active photosynthesis, and accumulation of biochemical compounds. These factors contribute to the expression of genetic potential and adaptation of the promising lines to local conditions.

Biometric and phenological studies revealed certain deviations between the Meghrashaghik genotype used as plant material and the regenerant lines in terms of the duration of transitions between phenophases and growth rates. While the periods from mass seedling emergence to male flower anthesis in the control and lines R1-1, R4-4, and R5-5 coincided, this period was shortened by 2-3 days in lines R2-2 and R3-3. Regarding female flowers, all regenerant lines flowered 1-2 days earlier than the control. Early flowering of female flowers also contributed to faster fruit maturation. The shortest vegetation period was recorded in lines R4-4 and R5-5, which was reduced by 2-3 days compared to other regenerant lines and by 4 days compared to the control (Table 2).

Table 2. Phenological observations

Genotype	* Average number of days from mass seedling emergence to		
	flowering of		fruit reaching technical maturity
	male flowers	female flowers	
Meghrashaghik (control)	44	53	92
R1-1	44	52	91
R2-2	41	52	90
R3-3	42	52	90
R4-4	44	51	88
R5-5	44	51	88

*Values rounded to the nearest whole number

In addition to the duration of plant vegetation, deviations were also observed in biometric traits of the regenerant lines compared to the control. An increasing trend in biometric parameters was noted in all regenerant lines, except for R1-1. The highest values for main stem length, number of lateral shoots, and assimilation area were recorded in lines R4-4 and R5-5, exceeding the control by 15.6%, 27.4%, and 37.3% for R4-4, and by 15.1%, 21.9%, and 34.6% for R5-5, respectively (Table 3).

Table 3. Growth and development of the studied melon lines

Genotype	Main stem length, cm ± SD	Number of shoots, pcs ± SD	Assimilation area, dm^2 ± SD	Dry mass per plant, g ± SD
Meghrashaghik (control)	282.5±18.5	7.3± 1.3	265.2± 5.4	302.6± 2.3
R1-1	275.7± 15.5	6.5± 1.4	262.2± 5.8	296.5± 2.0
R2-2	302.0± 17.4	7.6± 1.2	308.0± 5.3	321.0± 1.5
R3-3	310.0± 20.7	8.2± 1.4	326.1± 4.6	329.2± 1.3
R4-4	326.7±20.4	9.3± 1.6	364.2± 5.1	342.1± 2.1
R5-5	325.1± 22.0	8.9± 1.5	357.2± 4.9	333.5± 1.4

Compared to the control, the increased assimilation area of the regenerant lines, which naturally leads to enhanced photosynthetic activity, contributed to the intensive growth of aboveground organs, as indicated by the data in Table 3. The lowest dry matter accumulation per plant compared to the control was recorded in regenerant line R1-1. In contrast, all other regenerant lines exhibited a consistent increase in this parameter relative to the control. The highest dry matter accumulation per plant was observed in line R4-4, exceeding the control by 13.1%, followed by R5-5 (10.2%), R3-3 (8.8%), and R2-2 (6.1%).

Melon fruit size can vary considerably, ranging from very small (<100 g) to large and giant fruits (1–10 kg), while fruit shape varies from round to elongated. It is well established that fruit size and shape are genetically controlled traits and are determined at early stages of floral meristem development [33].

In all studied regenerant plants, no changes in fruit external appearance were observed compared to the control. Fruits of all genotypes were yellow-orange, oval-shaped, with a netted rind and thick, light cream-colored, crisp, and juicy flesh. However, despite the similarity in external morphology, the tested genotypes differed in fruit weight. Compared to the control (2.4 ± 0.2 kg), the highest fruit weight was recorded in regenerant lines R4-4 (2.7 ± 0.1 kg) and R5-5 (2.7 ± 0.3 kg), whereas the lowest fruit weight was observed in line R1-1 (2.2 ± 0.3 kg). In

lines R2-2 and R3-3, fruit weight did not differ significantly from that of the control.

According to recent studies, the development of new high-yielding melon cultivars requires the use of diverse genotypes as source material, including traditional cultivars and breeding lines, in order to integrate valuable traits. Available evidence indicates that many economically important characteristics, such as yield and fruit quality, are polygenically inherited and strongly influenced by growing conditions, highlighting the complexity of conventional breeding and the necessity of applying biotechnological approaches to improve its efficiency [34].

The results of our study showed that the highest yield (average values for 2023-2025) was recorded in lines R4-4 and R5-5, reaching 287.2 and 287.3 cwt·ha^{-1}, respectively. Compared to the control, these lines produced nearly identical yield increases of 9.3% and 9.4%. Relative to the control, regenerant lines R2-2 and R3-3 also exhibited moderate increases in total yield, amounting to 1.5% (266.5 cwt·ha^{-1}) and 1.8% (267.2 cwt·ha^{-1}), respectively. The lowest yield was observed in line R1-1 (243.8 cwt·ha^{-1}), which was 7.2% lower than that of the control (Table 4).

Table 4. Yield data of the studied melon lines (cwt·ha^{-1})

Genotype	Total yield, cwt·ha^{-1}				Marketable yield, cwt·ha^{-1}	Marketable yield, % of total	Increase relative to control
	2023	2024	2025	Average			
Meghrashaghik (control)	261.1	266.6	260.1	262.6	185.9	70.8	-
R1-1	241.5	244.5	245.5	243.8	160.4	65.8	-7.2
R2-2	266.0	266.8	266.7	266.5	191.3	71.8	+1.5
R3-3	267.8	266.8	266.9	267.2	196.7	73.6	+ 1.8
R4-4	287.8	287.4	286.4	287.2	231.5	80.6	+9.3
R5-5	288.3	287.3	286.4	287.3	217.8	75.8	+9.4
LSD_{05}	5.0	2.2	3.7	2.3			

All regenerant lines, except R1-1, were distinguished not only by higher yield but also by improved yield quality. The proportion of marketable yield within the total yield exceeded that of the control (70.8%) by 1.0%, 2.8%, 9.8%, and 5.0% in lines R2-2, R3-3, R4-4, and R5-5, respectively. Notably, although line R5-5 was comparable to R4-4 in terms of total and marketable yield, it contained 4.8% less marketable produce within the total yield, indicating a relative reduction in harvest quality compared with the best-performing line R4-4.

The climatic conditions of the Ararat Valley favored optimal melon development and the accumulation of biochemical compounds in the fruits. Average daily temperatures during the growing season (April-September 2023-2025) ranged from 19.7-25.0 °C in April-May to 34.9-36.2 °C in July-August, while night temperatures varied from 10.5-14.5 °C in spring to 21.8-22.9 °C in summer, creating diurnal fluctuations that were favorable for the formation of sugars and dry matter in the fruits.

Analysis of the data presented in Figures 2 and 3 revealed qualitative differences among the fruits of the regenerant lines. For instance, the dry matter content in fruits of R4-4 and R5-5 lines exceeded that of the control fruits by 7.4% and 2.5%, respectively, whereas the dry matter content in fruits of R2-2 and R3-3 lines was comparable to the control, and fruits of the R1-1 line showed a 7.4% decrease relative to the control (Fig. 2).

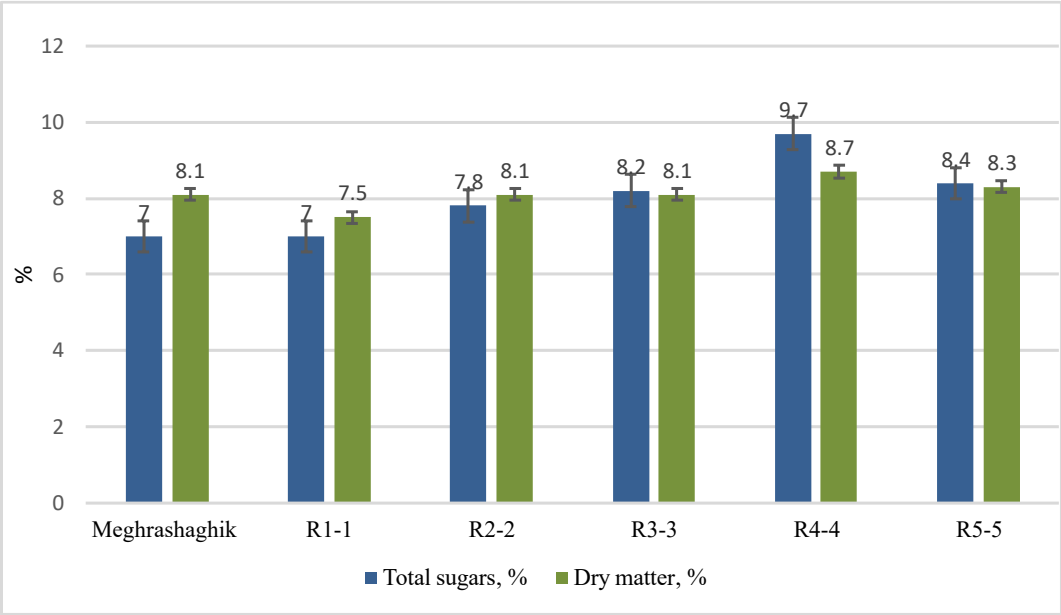


Figure 2. Total sugar and dry matter content in fruits of the studied melon lines ($p \leq 0.05$)

The sugar content in melon fruits is a critical determinant of quality and consumer value and represents one of the key breeding objectives. The main sugars include sucrose, glucose, and fructose, with sucrose accumulation at the later stages of fruit development playing a decisive role in increasing total sugar content. The metabolic pathway for sucrose accumulation involves approximately 20 enzymes, reflecting the complex genetic control of this trait [35]. According to numerous studies, although this trait is genetically determined, its expression is strongly influenced by growing conditions and the nutritional background [36].

Analysis of the study results revealed deviations in sugar content among the fruits of the regenerant lines, both relative to each other and to the control. Compared to the control, fruits of the R1-1 line accumulated a comparable amount of sugars (up to 7.0%), whereas fruits of R2-2, R3-3, and R5-5 showed an increasing trend, exceeding the control by 11.4% (up to 7.8%), 17.1% (up to 8.2%), and 20.0% (up to 8.4%), respectively. The highest sugar content was observed in the R4-4 line, at 9.7%, which is 38.5% higher than in the control (Fig. 2).

Our data are consistent with the results of international studies on the biochemical composition of various melon cultivars. In the study by Manchali (2021), conducted on 30 genotypes (including improved cultivars, landraces, and wild types), it was shown that soluble solids and sugar contents varied significantly, with landraces exhibiting the highest values for these traits [37].

Regarding another key quality trait, ascorbic acid content, the analysis of our samples also revealed notable variations. The lowest vitamin C content was observed in fruits of the R1-1 line (16.4 mg/%), which was 6.1% lower than the control. In contrast, all other regenerant lines accumulated relatively higher amounts of vitamin C than the control (17.4 mg/%), reaching a maximum in the fruits of the R4-4 line (20.1 mg/%, 15.5% above the control). In fruits of R2-2, R3-3, and R5-5 lines, vitamin C content exceeded that of the control by 6.3%, 8.6%, and 10.3%, respectively (Fig. 3). These findings are in agreement with the results of Buczkowska (2023), who reported that vitamin C content in melon fruits is largely determined by the genetic characteristics of the cultivars [38].

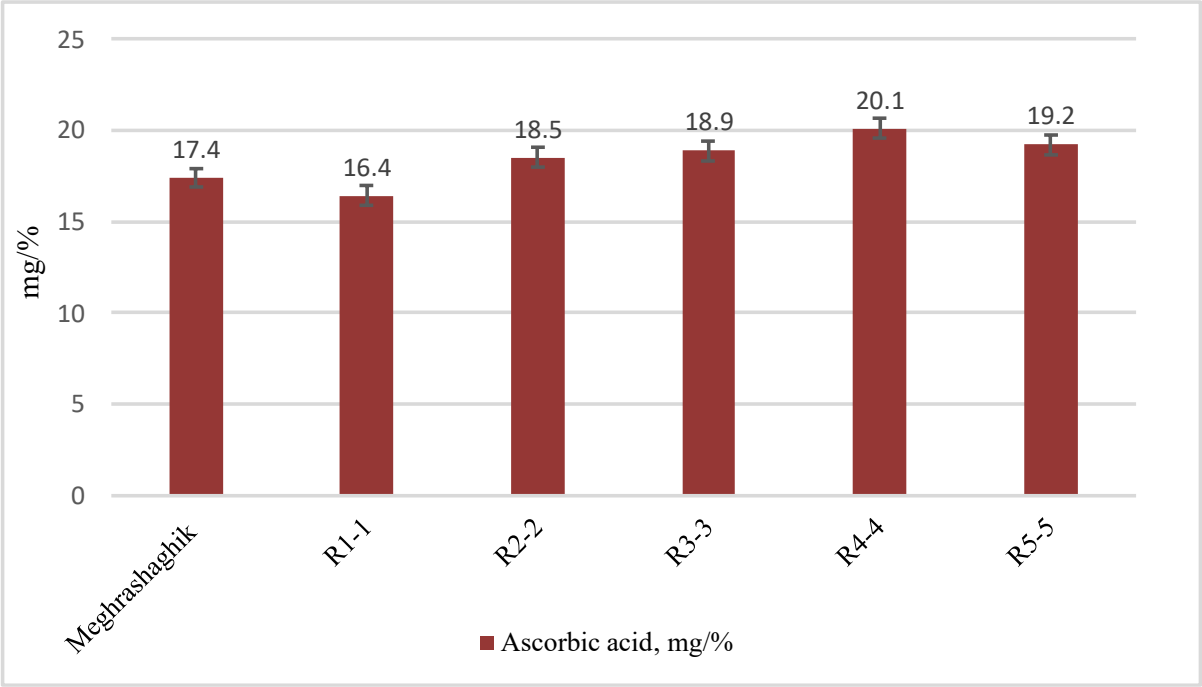


Figure 3. Ascorbic acid content in fruits of the studied genotypes ($p \leq 0.05$)

Based on the results of the study, the R4-4 and R5-5 regenerant lines were selected as starting material for further breeding, as they demonstrated superior performance in both quantitative and qualitative traits compared to the control and other regenerant lines. The identified regenerant lines with increased sugar and vitamin C content represent promising breeding material not only for productivity but also for functional food value. The higher levels of these bioactive compounds are directly associated with improved nutritional and antioxidant properties of the fruits. From the perspective of functional food concepts, such genotypes can be considered as a basis for developing new melon cultivars with enhanced nutritional quality.

CONCLUSION

The use of the landrace melon Meghrashaghik as the starting material in in vitro culture enabled the production of regenerants with high regeneration and rooting frequencies, exhibiting somaclonal variation as a source of genetic variability. Among the five promising lines, R4-4 and R5-5 demonstrated the highest values for biometric traits, accelerated vegetative growth, yield, and fruit quality. These lines possess a combination of agronomically valuable traits and can be used in breeding programs to develop high-yielding, high-quality melon cultivars. The obtained results highlight the potential of biotechnological approaches in melon breeding for the accelerated generation of diverse genotypic material and the expansion of breeding programs.

List of abbreviations: SCVIC- Scientific Center of Vegetable and Industrial Crops; MEofRA – Ministry of Economy of the Republic of Armenia; MS- Murashige and Skoog; BA - 6-Benzylaminopurine; NAA- α-Naphthaleneacetic acid; IAA- Indole-3-acetic acid; IBA-Indole-3-butyric acid

Competing interests: The authors declare that they have no financial, professional, or personal competing interests that could have appeared to influence the work reported in this manuscript.

Authors' contributions: AP conceived and designed the study. IV, ZH, and HM performed the biotechnological

and biochemical analyses and interpreted the data. RB, LT, AH, and AP conducted field experiments and collected and processed the agronomic data. GS and ITs handled data processing and provided resources. AA supplied seeds from the gene bank and participated in data processing. All authors read and approved the final version of the manuscript.

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